

SEQUENCE LISTING

<110> Japan Science And Technology Corporation

<120> Nicotianamine synthase, genes coding nicotianamine synthase

<130> PA906235

<160> 22

<210> 1

<211> 328

<212> PRT

<213> Hordeum vulgare L.

<400> 1

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Ser	Pro	Glu	Val	Asp	Arg	Leu	Phe	Thr	Asp	Leu	Val	Thr	Ala	Cys	45
Val	Pro	Pro	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Ser	Pro	Glu	His	60
Gln	Arg	Met	Arg	Glu	Ala	Leu	Ile	Arg	Leu	Cys	Ser	Ala	Ala	Glu	75
Gly	Lys	Leu	Glu	Ala	His	Tyr	Ala	Asp	Leu	Leu	Ala	Thr	Phe	Asp	90
Asn	Pro	Leu	Asp	His	Leu	Gly	Leu	Phe	Pro	Tyr	Tyr	Ser	Asn	Tyr	105
Val	Asn	Leu	Ser	Arg	Leu	Glu	Tyr	Glu	Leu	Leu	Ala	Arg	His	Val	120
Pro	Gly	Ile	Ala	Pro	Ala	Arg	Val	Ala	Phe	Val	Gly	Ser	Gly	Pro	135
Leu	Pro	Phe	Ser	Ser	Leu	Val	Leu	Ala	Ala	His	His	Leu	Pro	Glu	150
Thr	Gln	Phe	Asp	Asn	Tyr	Asp	Leu	Cys	Gly	Ala	Ala	Asn	Glu	Arg	165
Ala	Arg	Lys	Leu	Phe	Gly	Ala	Thr	Ala	Asp	Gly	Val	Gly	Ala	Arg	180
Met	Ser	Phe	His	Thr	Ala	Asp	Val	Ala	Asp	Leu	Thr	Gln	Glu	Leu	195
Gly	Ala	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Ala	210
Ala	Glu	Glu	Lys	Ala	Lys	Val	Ile	Ala	His	Leu	Gly	Ala	His	Met	225
Val	Glu	Gly	Ala	Ser	Leu	Val	Val	Arg	Ser	Ala	Arg	Pro	Arg	Gly	240
Phe	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Glu	Asp	Ile	Arg	Arg	Gly	Gly	255
Phe	Glu	Val	Leu	Ala	Val	His	His	Pro	Glu	Gly	Glu	Val	Ile	Asn	270
Ser	Val	Ile	Val	Ala	Arg	Lys	Ala	Val	Glu	Ala	Gln	Leu	Ser	Gly	285
Pro	Gln	Asn	Gly	Asp	Ala	His	Ala	Arg	Gly	Ala	Val	Pro	Leu	Val	300
Ser	Pro	Pro	Cys	Asn	Phe	Ser	Thr	Lys	Met	Glu	Ala	Ser	Ala	Leu	315
Glu	Lys	Ser	Glu	Glu	Leu	Thr	Ala	Lys	Glu	Leu	Ala	Phe			328

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<211> 1295

<212> DNA

<213> Hordeum vulgare L.

<400> 2

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GCCCAGAACAA	AGGAGGTCGC	TGCTCTGATC	GAGAAGATCG	CCGGTATCCA	GGCCGCCATC
130	140	150	160	170	180
GCCGAGCTGC	CGTCGCTGAG	CCCGTCCCCC	GAGGTCGACA	GGCTCTTCAC	CGACCTCGTC
190	200	210	220	230	240
ACGGCCTGCG	TCCCGCCGAG	CCCCGTCGAC	GTGACGAAGC	TCAGCCCGGA	GCACCAGAGG

250	260	270	280	290	300
ATGCGGGAGG	CTCTCATCCG	CTTGTGCTCC	GCCGCCGAGG	GGAAGCTCGA	GGCGCACTAC
310	320	330	340	350	360
GCCGACCTGC	TCGCCACCTT	CGACAACCCG	CTCGACCACC	TCGGCCTCTT	CCCGTACTAC
370	380	390	400	410	420
AGCAACTACG	TCAACCTCAG	CAGGCTGGAG	TACGAGCTCC	TGGCGCGCCA	CGTGCCGGGC
430	440	450	460	470	480
ATCGCGCCGG	CGCGCGTCGC	CTTCGTCGGC	TCCGGCCCCG	TGCCGTTTCA	CTCGCTCGTC
490	500	510	520	530	540
CTCGCCGCGC	ACCACCTGCC	CGAGACCCAG	TTCGACAACT	ACGACCTGTG	CGGCGCGGCC
550	560	570	580	590	600
AACGAGCGCG	CCAGGAAGCT	GTTCGGCGCG	ACGGCGGACG	GCGTCGGCGC	GCGTATGTCT
610	620	630	640	650	660
TTCACACCGG	CGGACGTCGC	CGACCTCACC	CAGGAGCTCG	GCGCCTACGA	CGTGGTCTTC
670	680	690	700	710	720
CTCGCCGCGC	TCGTCGGCAT	GGCAGCCGAG	GAGAAGGCCA	AGGTGATTGC	CCACCTGGGC
730	740	750	760	770	780
GCGCACATGG	TGGAGGGGGC	GTCCCTGGTC	GTGCGGAGCG	CACGGCCCCG	CGGCTTTCTT
790	800	810	820	830	840
TACCCCATTTG	TCGACCCGGA	GGACATCAGG	CGGGGTGGGT	TCGAGGTGCT	GGCCGTGCAC
850	860	870	880	890	900
CACCCGGAAG	GTGAGGTGAT	CAACTCTGTC	ATCGTCGCCC	GTAAGGCCGT	CGAAGCGCAG
910	920	930	940	950	960
CTCAGTGGGC	CGCAGAACGG	AGACGCGCAC	GCACGGGGCG	CGGTGCCGTT	GGTCAGCCCC
970	980	990	1000	1010	1020
CCATGCAACT	TCTCCACCAA	GATGGAGGCG	AGCGCGCTTG	AGAAGAGCGA	GGAGCTGACC
1030	1040	1050	1060	1070	1080
GCCAAAGAGC	TGGCCTTTTG	ATTGAAGAGT	GCGCGTGGTC	ATTCTGTCGC	CTGCGATCGT
1090	1100	1110	1120	1130	1140
GGTAACTTTT	CTACTCGTGT	GTGTTTTGAT	GTTTGTGCCT	GTAAGAGTTA	TGCTTCCGGC
1150	1160	1170	1180	1190	1200
CTTGTGCTGT	TAATTTACAC	GCGTTACATG	TAGTACTTGT	ATTTATACCT	GGAATAACGG
1210	1220	1230	1240	1250	1260
TATGTAACAT	AAATATTAGT	GGGATTTGAA	GTGTAATGCT	AAATAATAAG	AAAACCTTGT
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<211> 335
 <212> PRT
 <213> Hordeum vulgare L.
 <400> 3

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Pro	Ser	Pro	Asp	Val	Asp	Ala	Leu	Phe	Thr	Glu	Leu	Val	Thr	Ala	45
Cys	Val	Pro	Pro	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Gly	Pro	Glu	60
Ala	Gln	Glu	Met	Arg	Glu	Gly	Leu	Ile	Arg	Leu	Cys	Ser	Glu	Ala	75
Glu	Gly	Lys	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Ala	Ala	Phe	90
Asp	Lys	Pro	Leu	Asp	His	Leu	Gly	Met	Phe	Pro	Tyr	Tyr	Asn	Asn	105
Tyr	Ile	Asn	Leu	Ser	Lys	Leu	Glu	Tyr	Glu	Leu	Leu	Ala	Arg	Tyr	120
Val	Pro	Gly	Gly	Tyr	Arg	Pro	Ala	Arg	Val	Ala	Phe	Ile	Gly	Ser	135
Gly	Pro	Leu	Pro	Phe	Ser	Ser	Phe	Val	Leu	Ala	Ala	Arg	His	Leu	150
Pro	Asp	Thr	Met	Phe	Asp	Asn	Tyr	Asp	Leu	Cys	Gly	Ala	Ala	Asn	165
Asp	Arg	Ala	Ser	Lys	Leu	Phe	Arg	Ala	Asp	Arg	Asp	Val	Gly	Ala	180
Arg	Met	Ser	Phe	His	Thr	Ala	Asp	Val	Ala	Asp	Leu	Ala	Gly	Glu	195
Leu	Ala	Lys	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	210
Ala	Ala	Glu	Asp	Lys	Ala	Lys	Val	Ile	Ala	His	Leu	Gly	Ala	His	225
Met	Ala	Asp	Gly	Ala	Ala	Leu	Val	Val	Arg	Ser	Ala	His	Gly	Ala	240
Arg	Gly	Phe	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Gln	Asp	Ile	Gly	Arg	255
Gly	Gly	Phe	Glu	Val	Leu	Ala	Val	Cys	His	Pro	Asp	Asp	Asp	Val	270
Val	Asn	Ser	Val	Ile	Ile	Ala	Gln	Lys	Ser	Lys	Asp	Val	His	Ala	285
Asp	Gly	Leu	Gly	Ser	Gly	Arg	Gly	Ala	Gly	Gly	Gln	Tyr	Ala	Arg	300
Gly	Thr	Val	Pro	Val	Val	Ser	Pro	Pro	Cys	Arg	Phe	Gly	Glu	Met	315
Val	Ala	Asp	Val	Thr	Gln	Asn	His	Lys	Arg	Asp	Glu	Phe	Ala	Asn	330
Ala	Glu	Val	Ala	Phe											335

<210> 4
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 <212> DNA
 <213> Hordeum vulgare L.
 <400> 4

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GAGGTGGATG	CCCTGGTGGA	GAAGATCACC	GGGCTCCATG	CCGCAATCGC	CAAGCTGCCG
130	140	150	160	170	180
TCGCTCAGCC	CATCCCCGGA	CGTCGACGCG	CTCTTCACGG	AGCTGGTCAC	GGCGTGCGTT
190	200	210	220	230	240
CCACCGAGTC	CAGTGGACGT	GACCAAGCTC	GGGCCGGAGG	CGCAGGAGAT	GCGGGAGGGC
250	260	270	280	290	300
CTCATCCGCC	TATGCTCCGA	GGCCGAGGGG	AAGCTGGAGG	CGCACTACTC	CGACATGCTC
310	320	330	340	350	360
GCCGCCTTCG	ACAAGCCGCT	GGATCACCTC	GGCATGTTCC	CCTACTACAA	CAACTACATC
370	380	390	400	410	420
AACCTCAGCA	AGCTCGAGTA	CGAGCTCCTG	GCCCGCTACG	TGCCTGGCGG	CTATCGCCCCG

430	440	450	460	470	480
GCGCGCGTCG	CGTTCATCGG	CTCCGGCCCCG	CTGCCGTTCA	GCTCCTTTGT	CCTGGCCGCG
490	500	510	520	530	540
CGCCACCTGC	CCGACACCAT	GTTTCGACAAC	TATGACCTGT	GCGGTGCGGC	CAACGATCGC
550	560	570	580	590	600
GCCAGCAAGC	TCTTCCGCGC	GGATCGCGAC	GTGGGTGCCC	GCATGTCGTT	CCACACGGCC
610	620	630	640	650	660
GACGTCGCGG	ACCTCGCCGG	CGAGCTCGCC	AAGTACGACG	TTGTCTTCCT	GGCCGCACTC
670	680	690	700	710	720
GTCGGCATGG	CCGCCGAGGA	CAAGGCGAAG	GTGATCGCGC	ACCTCGGCGC	ACACATGGCA
730	740	750	760	770	780
GACGGGGCGG	CCCTCGTCGT	GCGCAGCGCA	CACGGAGCGC	GCGGGTTCCT	GTACCCGATC
790	800	810	820	830	840
GTCGACCCCC	AGGACATCGG	CCGAGGCGGG	TTGAGGTGC	TGGCCGTGTG	CCATCCCGAC
850	860	870	880	890	900
GACGACGTGG	TGAACTCCGT	CATCATCGCA	CAGAAGTCCA	AGGACGTGCA	TGCCGATGGA
910	920	930	940	950	960
CTTGGCAGCG	GGCGTGGTGC	CGGTGGACAG	TACGCGCGGG	GCACGGTGCC	TGTTGTCAGC
970	980	990	1000	1010	1020
CCCCCGTGCA	GGTTCGGCGA	GATGGTGGCG	GACGTGACCC	AGAACCACAA	GAGAGACGAG
1030	1040	1050	1060	1070	1080
TTTGCCAACG	CCGAAGTGGC	CTTTTGATCG	TTGCTGCGCA	GGGTGTGCAT	CCATGATCCA
1090	1100	1110	1120	1130	1140
TCCATACCTC	GTTCTGTGAT	TGCATCAAGC	TTGCAATCGT	ATGCATTTCA	AGTCACGTGT
1150	1160	1170	1180	1190	1200
TGCTTCTATC	CAATAATGTA	CGTGTGGTGT	TTACACGCGA	ATGTCTTGTA	GACCTTTGTA
1210	1220	1230	1240	1250	1260
TGTGTACAAG	TGAATTTTAA	TTCACAAGTA	CATATAATGG	TCACCATTGA	AAAGATGTTT
1270	1280	1290	1300	1310	1320
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<210> 5

<211> 335

<212> PRT

<213> Hordeum vulgare L.

<400> 5

Met Ala Ala Gln Asn Asn Asn Lys Asp Val Ala Ala Leu Val Glu
Lys Ile Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu

15

30

Ser	Pro	Ser	Pro	Asp	Val	Asp	Ala	Leu	Phe	Thr	Glu	Leu	Val	Thr	45
Ala	Cys	Val	Pro	Pro	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Gly	Pro	60
Glu	Ala	Gln	Glu	Met	Arg	Glu	Gly	Leu	Ile	Arg	Leu	Cys	Ser	Glu	75
Ala	Glu	Gly	Lys	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Ala	Ala	90
Phe	Asp	Asn	Pro	Leu	Asp	His	Leu	Gly	Ile	Phe	Pro	Tyr	Tyr	Ser	105
Asn	Tyr	Ile	Asn	Leu	Ser	Lys	Leu	Glu	Tyr	Glu	Leu	Leu	Ala	Arg	120
Tyr	Val	Arg	Arg	His	Arg	Pro	Ala	Arg	Val	Ala	Phe	Ile	Gly	Ser	135
Gly	Pro	Leu	Pro	Phe	Ser	Ser	Phe	Val	Leu	Ala	Ala	Arg	His	Leu	150
Pro	Asp	Thr	Met	Phe	Asp	Asn	Tyr	Asp	Leu	Cys	Gly	Ala	Ala	Asn	165
Asp	Arg	Ala	Ser	Lys	Leu	Phe	Arg	Ala	Asp	Thr	Asp	Val	Gly	Ala	180
Arg	Met	Ser	Phe	His	Thr	Ala	Asp	Val	Ala	Asp	Leu	Ala	Ser	Glu	195
Leu	Ala	Lys	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	210
Ala	Ala	Glu	Asp	Lys	Ala	Lys	Val	Ile	Ala	His	Leu	Gly	Ala	His	225
Met	Ala	Asp	Gly	Ala	Ala	Leu	Val	Val	Arg	Ser	Ala	His	Gly	Ala	240
Arg	Gly	Phe	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Gln	Asp	Ile	Gly	Arg	255
Gly	Gly	Phe	Glu	Val	Leu	Ala	Val	Cys	His	Pro	Asp	Asp	Asp	Val	270
Val	Asn	Ser	Val	Ile	Ile	Ala	Gln	Lys	Ser	Lys	Glu	Val	His	Ala	285
Asp	Gly	Leu	Gly	Ser	Ala	Arg	Gly	Ala	Gly	Arg	Gln	Tyr	Ala	Arg	300
Gly	Thr	Val	Pro	Val	Val	Ser	Pro	Pro	Cys	Arg	Phe	Gly	Glu	Met	315
Val	Ala	Asp	Val	Thr	Gln	Asn	His	Lys	Arg	Asp	Glu	Phe	Ala	Asn	330
Ala	Glu	Val	Ala	Phe											335

<210> 6

<211> 1314

<212> DNA

<213> Hordeum vulgare L.

<400> 6

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130	140	150	160	170	180
CGTCGCTCAG	CCCATCCCCG	GACGTGACG	CGCTCTTCAC	CGAGCTGGTC	ACGGCGTGCG
190	200	210	220	230	240
TTCCCCCGAG	CCCCGTGGAC	GTGACCAAGC	TCGGCCCCGA	GGCGCAGGAG	ATGCGGGAGG
250	260	270	280	290	300
GCCTCATCCG	CCTCTGCTCC	GAGGCCGAGG	GGAAGCTGGA	GGCGCACTAC	TCCGACATGC
310	320	330	340	350	360
TCGCCGCCCTT	CGACAACCCG	CTGGATCACC	TCGGCATCTT	CCCCTACTAC	AGCAACTACA
370	380	390	400	410	420
TCAACCTCAG	CAAGCTGGAG	TACGAGCTCC	TGGCACGCTA	CGTCCGGCGG	CATCGCCCCG
430	440	450	460	470	480
CCCGCGTCGC	GTTTCATCGG	TCCGGCCCCG	TGCCGTTTCA	CTCCTTTGTC	CTGGCCGCGC
490	500	510	520	530	540
GCCACCTGCC	CGACACCATG	TTTGACAACT	ACGACCTTTG	CGGCGCGGCC	AACGATCGCG
550	560	570	580	590	600
CCAGCAAGCT	CTTCCGCGCG	GACACGGACG	TGGGTGCCCC	CATGTCGTTC	CACACGGCCG

610	620	630	640	650	660
ACGTCGCGGA	CCTCGCCAGC	GAGCTCGCCA	AGTACGACGT	CGTCTTCCTG	GCCGCGCTCG
670	680	690	700	710	720
TCGGCATGGC	CGCCGAGGAC	AAGGCCAAGG	TGATCGCGCA	CCTCGGCGCA	CACATGGCAG
730	740	750	760	770	780
ACGGGGCGGC	CCTCGTCGTG	CGCAGCGCAC	ACGGAGCGCG	CGGGTTCCTG	TACCCGATTG
790	800	810	820	830	840
TCGACCCCCA	GGACATCGGC	CGCGGCGGGT	TCGAGGTGCT	GGCCGTGTGC	CACCCCGACG
850	860	870	880	890	900
ACGACGTGGT	GAATCCGTC	ATCATCGCAC	AGAAGTCCAA	GGAGGTGCAT	GCCGATGGAC
910	920	930	940	950	960
TTGGCAGCGC	GCGTGGTGCC	GGTCGACAGT	ACGCGCGCGG	CACGGTGCCG	GTTGTCAGCC
970	980	990	1000	1010	1020
CCCCGTGCAG	GTTCCGGTGAG	ATGGTGGCGG	ATGTGACCCA	GAACCACAAG	AGAGACGAGT
1030	1040	1050	1060	1070	1080
TTGCCAACGC	CGAAGTGGCC	TTTTGATCGA	TCGTGCGCAA	GGGACAATAA	ATGAACGTGG
1090	1100	1110	1120	1130	1140
ATGTGGTAGG	GTAATTTGCC	TACCTCGCTG	CTTGATCGCT	TGCAATATGT	GCACATTTTC
1150	1160	1170	1180	1190	1200
CTACTACCGC	TGCTTATGCA	TTTCAAGCCA	TGTGATGTTG	GTATCCAATA	AAGTATGTGT
1210	1220	1230	1240	1250	1260
AGGGTTTACA	CGCAAATGTC	TTTACACCTT	GTACGTGTAA	GTGTTGACAA	CGATGAATTT
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<210> 7

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<212> PRT

<213> Hordeum vulgare L.

<400> 7

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Thr	Gly	Leu	His	Ala	Ala	Ile	Ala	Lys	Leu	Pro	Ser	Leu	Ser	Pro	30
Ser	Pro	Asp	Val	Asp	Ala	Leu	Phe	Thr	Asp	Leu	Val	Thr	Ala	Cys	45
Val	Pro	Pro	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Ala	Pro	Glu	Ala	60
Gln	Ala	Met	Arg	Glu	Gly	Leu	Ile	Arg	Leu	Cys	Ser	Glu	Ala	Glu	75
Gly	Lys	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Ala	Ala	Phe	Asp	90
Asn	Pro	Leu	Asp	His	Leu	Gly	Val	Phe	Pro	Tyr	Tyr	Ser	Asn	Tyr	105
Ile	Asn	Leu	Ser	Lys	Leu	Glu	Tyr	Glu	Leu	Leu	Ala	Arg	Tyr	Val	120
Pro	Gly	Arg	His	Arg	Pro	Ala	Arg	Val	Ala	Phe	Ile	Gly	Ser	Gly	135
Pro	Leu	Pro	Phe	Ser	Ser	Tyr	Val	Leu	Ala	Ala	Arg	His	Leu	Pro	150
Asp	Thr	Val	Phe	Asp	Asn	Tyr	Asp	Leu	Cys	Gly	Ala	Ala	Asn	Asp	165
Arg	Ala	Thr	Arg	Leu	Phe	Arg	Ala	Asp	Lys	Asp	Val	Gly	Ala	Arg	180
Met	Ser	Phe	His	Thr	Ala	Asp	Val	Ala	Asp	Leu	Thr	Asp	Glu	Leu	195

Ala Thr Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala	210
Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala His Met	225
Ala Asp Gly Ala Ala Leu Val Ala Arg His Gly Ala Arg Gly Phe	240
Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly Phe	255
Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn Ser	270
Val Ile Ile Ala Gln Lys Ser Asn Asp Val His Glu Tyr Gly Leu	285
Gly Ser Gly Arg Gly Gly Arg Tyr Ala Arg Gly Thr Val Val Pro	300
Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val	315
Thr Gln Lys Arg Glu Glu Phe Ala Asn Ala Glu Val Ala Phe	329

<210> 8

<211> 1249

<212> DNA

<213> *Hordeum vulgare* L.

<400> 8

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ACATAAAAAT	GGACGGCCAG	AGCGAGGAGG	TCGACGCCCT	TGTCCAGAAG	ATCACCGGCC
130	140	150	160	170	180
TCCACGCCGC	CATCGCCAAG	CTGCCCTCGC	TCAGCCCGTC	CCCGGACGTC	GACGCGCTCT
190	200	210	220	230	240
TCACCGACCT	GGTCACCGCG	TGCGTGCCCC	CGAGCCCCGT	GGACGTGACC	AAGCTCGCCC
250	260	270	280	290	300
CGGAGGCGCA	GGCGATGCGG	GAGGGCCTCA	TCCGCCTCTG	CTCCGAGGCC	GAGGGCAAGC
310	320	330	340	350	360
TGGAGGCGCA	CTACTCCGAC	ATGCTCGCCG	CCTTCGACAA	CCCGCTCGAC	CACCTCGGCG
370	380	390	400	410	420
TCTTCCCCTA	CTACAGCAAC	TACATCAACC	TCAGCAAGCT	TGAGTACGAG	CTCCTCGCGC
430	440	450	460	470	480
GCTACGTGCC	CGGCAGGCAT	CGCCCGGCCC	GCGTCGCCTT	CATCGGCTCC	GGCCCGCTGC
490	500	510	520	530	540
CGTTCAGCTC	CTACGTCTC	GCCGCGCGCC	ACCTGCCCGA	CACCGTGTTC	GACAACTACG
550	560	570	580	590	600
ACCTGTGCGG	CGCGGCCAAC	GACCGCGCGA	CCAGGCTGTT	CCGCGCGGAC	AAGGACGTCG
610	620	630	640	650	660
GCGCCCGCAT	GTCGTTCCAC	ACCGCCGACG	TCGCGGACCT	CACCGACGAG	CTCGCTACGT
670	680	690	700	710	720
ACGACGTCGT	CTTCCTGGCC	GCGCTCGTGG	GCATGGCCGC	CGAGGACAAG	GCCAAGGTGA
730	740	750	760	770	780
TCGCGCACCT	TGGCGCGCAC	ATGGCGGACG	GGGCGGCCCT	CGTTGCGCGG	CACGGCGCGC
790	800	810	820	830	840
GTGGGTTCTT	CTACCCGATC	GTCGATCCCC	AGGACATCGG	TCGAGGCGGG	TTCGAGGTGC

850 860 870 880 890 900
 TCGCCGTGTG TCACCCCGAC GACGACGTGG TGAACCTCCGT CATCATCGCA CAAAAGAGCA
 910 920 930 940 950 960
 ACGACGTGCA CGAGTATGGA CTTGGCAGCG GGCGTGTTGG ACGGTACGCG CGAGGCACGG
 970 980 990 1000 1010 1020
 TGGTGCCGGT GGTCAGCCCA CCCTGCAGGT TCGGCGAGAT GGTGGCAGAC GTGACCCAGA
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 AGAGAGAGGA GTTTGCCAAC GCGGAAGTGG CCTTCTGATT GCTGCTGAAT CGCTTGTGAT
 1090 1100 1110 1120 1130 1140
 CGTACGTGGT AATTTTTTCTA CTACTCCTCC TCCTACCACC ACCTATCACC TATGTATGCA
 1150 1160 1170 1180 1190 1200
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<210> 9
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 <213> Hordeum vulgare L.
 <400> 9

Met	Glu	Ala	Glu	Asn	Gly	Glu	Val	Ala	Ala	Leu	Val	Glu	Lys	Ile	15
Thr	Gly	Leu	His	Ala	Ala	Ile	Ser	Lys	Leu	Pro	Ala	Leu	Ser	Pro	30
Ser	Pro	Gln	Val	Asp	Ala	Leu	Phe	Thr	Glu	Leu	Val	Ala	Ala	Cys	45
Val	Pro	Ser	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Gly	Pro	Glu	Ala	60
Gln	Glu	Met	Arg	Gln	Asp	Leu	Ile	Arg	Leu	Cys	Ser	Ala	Ala	Glu	75
Gly	Leu	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Thr	Ala	Leu	Asp	90
Ser	Pro	Leu	Asp	His	Leu	Gly	Arg	Phe	Pro	Tyr	Phe	Asp	Asn	Tyr	105
Val	Asn	Leu	Ser	Lys	Leu	Glu	His	Asp	Leu	Leu	Ala	Gly	His	Val	120
Ala	Ala	Pro	Ala	Arg	Val	Ala	Phe	Ile	Gly	Ser	Gly	Pro	Leu	Pro	135
Phe	Ser	Ser	Leu	Phe	Leu	Ala	Thr	Tyr	His	Leu	Pro	Asp	Thr	Arg	150
Phe	Asp	Asn	Tyr	Asp	Arg	Cys	Ser	Val	Ala	Asn	Gly	Arg	Ala	Met	165
Lys	Leu	Val	Gly	Ala	Ala	Asp	Glu	Gly	Val	Arg	Ser	Arg	Met	Ala	180
Phe	His	Thr	Ala	Glu	Val	Thr	Asp	Leu	Thr	Ala	Glu	Leu	Gly	Ala	195
Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Thr	Ser	Lys	210
Glu	Lys	Ala	Asp	Ala	Ile	Ala	His	Leu	Gly	Lys	His	Met	Ala	Asp	225
Gly	Ala	Val	Leu	Val	Arg	Glu	Ala	Leu	His	Gly	Ala	Arg	Ala	Phe	240
Leu	Tyr	Pro	Val	Val	Glu	Leu	Asp	Asp	Val	Gly	Arg	Gly	Gly	Phe	255
Gln	Val	Leu	Ala	Val	His	His	Pro	Ala	Gly	Asp	Glu	Val	Phe	Asn	270
Ser	Phe	Ile	Val	Ala	Arg	Lys	Val	Lys	Met	Ser	Ala				282

<210> 10
 <211> 1044
 <212> DNA
 <213> Hordeum vulgare L.
 <400> 10

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70	80	90	100	110	120
ACGCCGCCAT	CTCCAAGCTC	CCGGCACTAA	GCCCGTCTCC	TCAAGTCGAC	GCGCTCTTCA
130	140	150	160	170	180
CCGAGCTGGT	TGCGGCGTGC	GTCCCATCAA	GCCCGGTGGA	CGTGACCAAG	CTCGGCCCGG
190	200	210	220	230	240
AGGCGCAGGA	GATGCGGCAG	GACCTCATCC	GTCTCTGCTC	GGCCGCCGAG	GGGCTGCTCG
250	260	270	280	290	300
AGGCGCACTA	CTCCGACATG	CTCACCGCGT	TGGACAGCCC	GCTCGACCAC	CTCGGCCCGT
310	320	330	340	350	360
TCCCTTACTT	CGACAAC TAC	GTCAACCTCA	GCAAGCTCGA	GCACGATCTT	CTGGCAGGTC
370	380	390	400	410	420
ACGTGGCGGC	CCCGGCCCGC	GTGGCGTTCA	TCGGGTCGGG	GCCACTGCCG	TTCAGCTCGC
430	440	450	460	470	480
TCTTCCTTGC	GACGTACCAC	CTGCCGGACA	CCCGGTTCTGA	CAACTACGAC	CGGTGCAGCG
490	500	510	520	530	540
TGGCGAATGG	CCGGGCGGATG	AAGCTGGTGC	GCGCGGCGGA	CGAGGGCGTG	CGATCACGCA
550	560	570	580	590	600
TGGCGTTCCA	CACGGCCGAA	GTCACGGACC	TCACGGCTGA	GCTCGGCGCT	TACGACGTGG
610	620	630	640	650	660
TCTTCCTGGC	CGCGCTCGTG	GGAATGACGT	CCAAGGAGAA	GGCCGACGCC	ATAGCGCACT
670	680	690	700	710	720
TGGGGAAGCA	CATGGCAGAT	GGGGCGGTGC	TCGTGCGCGA	AGCGCTGCAC	GGGGCGCGAG
730	740	750	760	770	780
CGTTCCTGTA	TCCTGTCTGTG	GAGCTGGACG	ATGTCGGGCG	TGGTGGGTTC	CAAGTGCTGG
790	800	810	820	830	840
CCGTGCACCA	CCCTGCAGGC	GATGAGGTGT	TCAACTCATT	CATAGTTGCC	CGGAAGGTGA
850	860	870	880	890	900
AAATGAGTGC	TTAAATTAAG	AAAAGGGTGA	GCCTGTCTGC	TTGTGCAAAT	GGTGTCTCAC
910	920	930	940	950	960
ATTGATAATA	ACCAGATGAT	ACCCTGCACA	TTGATGGGGG	TACTGCAGTA	TGTTTCAATG
970	980	990	1000	1010	1020
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<210> 11

<211> 328

<212> PRT

<213> Hordeum vulgare L.

<400> 11

Met	Asp	Ala	Gln	Asn	Lys	Glu	Val	Asp	Ala	Leu	Val	Gln	Lys	Ile	15
Thr	Gly	Leu	His	Ala	Ala	Ile	Ala	Lys	Leu	Pro	Ser	Leu	Ser	Pro	30
Ser	Pro	Asp	Val	Asp	Ala	Leu	Phe	Thr	Asp	Leu	Val	Thr	Ala	Cys	45
Val	Pro	Pro	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Gly	Ser	Glu	Ala	60
Gln	Glu	Met	Arg	Glu	Gly	Leu	Ile	Arg	Leu	Cys	Ser	Glu	Ala	Glu	75
Gly	Lys	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Ala	Ala	Phe	Asp	90
Asn	Pro	Leu	Asp	His	Leu	Gly	Met	Phe	Pro	Tyr	Tyr	Ser	Asn	Tyr	105
Ile	Asn	Leu	Ser	Lys	Leu	Glu	Tyr	Glu	Leu	Leu	Ala	Arg	Tyr	Val	120
Pro	Gly	Gly	Ile	Ala	Arg	Pro	Ala	Val	Ala	Phe	Ile	Gly	Ser	Gly	135
Pro	Leu	Pro	Phe	Ser	Ser	Tyr	Val	Leu	Ala	Ala	Arg	His	Leu	Pro	150
Asp	Ala	Met	Phe	Asp	Asn	Tyr	Asp	Leu	Cys	Ser	Ala	Ala	Asn	Asp	165
Arg	Ala	Ser	Lys	Leu	Phe	Arg	Ala	Asp	Lys	Asp	Val	Gly	Ala	Arg	180
Met	Ser	Phe	His	Thr	Ala	Asp	Val	Ala	Asp	Leu	Thr	Arg	Glu	Leu	195
Ala	Ala	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Ala	210
Ala	Glu	Asp	Lys	Ala	Lys	Val	Ile	Pro	His	Leu	Gly	Ala	His	Met	225
Ala	Asp	Gly	Ala	Ala	Leu	Val	Val	Arg	Ser	Ala	Gln	Ala	Arg	Gly	240
Phe	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Gln	Asp	Ile	Gly	Arg	Gly	Gly	255
Phe	Glu	Val	Leu	Ala	Val	Cys	His	Pro	Asp	Asp	Asp	Val	Val	Asn	270
Ser	Val	Ile	Ile	Ala	His	Lys	Ser	Lys	Asp	Val	His	Ala	Asn	Glu	285
Arg	Pro	Asn	Gly	Arg	Gly	Gly	Gln	Tyr	Arg	Gly	Ala	Val	Pro	Val	300
Val	Ser	Pro	Pro	Cys	Arg	Phe	Gly	Glu	Met	Val	Ala	Asp	Val	Thr	315
His	Lys	Arg	Glu	Glu	Phe	Thr	Asn	Ala	Glu	Val	Ala	Phe			328

<210> 12

<211> 1352

<212> DNA

<213> Hordeum vulgare L.

<400> 12

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70	80	90	100	110	120
AACAAGGAGG	TTGATGCCCT	GGTCCAGAAG	ATCACCGGCC	TCCACGCCGC	CATCGCCAAG
130	140	150	160	170	180
CTGCCGTCCC	TCAGCCCATC	ACCCGACGTC	GACGCGCTCT	TCACCGACCT	GGTCACCGCG
190	200	210	220	230	240
TGCGTCCCCC	CGAGCCCCGT	GGACGTGACC	AAGCTCGGGT	CGGAGGCGCA	GGAGATGCGG
250	260	270	280	290	300
GAGGGCCTCA	TCCGCCTCTG	CTCCGAGGCC	GAGGGGAAGC	TGGAGGCGCA	CTACTCCGAC
310	320	330	340	350	360
ATGCTGGCCG	CCTTCGACAA	CCCGCTCGAC	CACCTCGGCA	TGTTCCCCTA	CTACAGCAAC
370	380	390	400	410	420
TACATCAACC	TCAGCAAGCT	GGAGTACGAG	CTCCTGGCGC	GCTACGTGCC	GGGCGGCATC
430	440	450	460	470	480
GCCCGGCCCG	CTGTGCGGTT	CATCGGCTCC	GGCCCGCTGC	CGTTCAGCTC	CTACGTCTCT
490	500	510	520	530	540
GCCGCTCGCC	ACCTGCCCCA	CGCCATGTTT	GACAACTACG	ACCTGTGTAG	CGCGGCCAAT

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      550      560      570      580      590      600
GACCGTGC GA GCAAGCTGTT CCGCGCGGAC AAGGACGTGG GCGCCCGCAT GTCTTTCCAC

      610      620      630      640      650      660
ACCGCCGACG TAGCGGACCT CACCCGCGAG CTCGCCGCGT ACGACGTCGT CTTCTGGGCC

      670      680      690      700      710      720
GCGCTCGTGG GCATGGCTGC CGAGGACAAG GCCAAGGTGA TTCCGCACCT CGGCGCGCAC

      730      740      750      760      770      780
ATGGCGGACG GGGCGGCCCT CGTCGTGCGC AGTGCGCAGG CACGTGGGTT CCTCTACCCG

      790      800      810      820      830      840
ATCGTCGATC CCCAGGACAT CGGTCGAGGC GGGTTTGAGG TGCTGGCCGT GTGTCACCCC

      850      860      870      880      890      900
GACGATGACG TGGTGAAGTC CGTCATCATC GCACACAAGT CCAAGGACGT GCATGCCAAT

      910      920      930      940      950      960
GAACGTCCCA ACGGGCGTGG TGGACAGTAC CGGGGCGCGG TACCGGTGGT CAGCCCGCCG

      970      980      990      1000      1010      1020
TGCAGGTTTC GTGAGATGGT GGCGGACGTG ACCCACAAGA GAGAGGAGTT CACCAACGCG

      1030      1040      1050      1060      1070      1080
GAAGTGGCCT TCTGATCGTT GCGAGGGAAT GAAAATGAAG GTGGACGTGT GTGGTCAGCA

      1090      1100      1110      1120      1130      1140
TCCATACGTG GCTGCCTGCT TCATCGCTTG CAATCGTACT ACTACCTACC TATGCAGTTC

      1150      1160      1170      1180      1190      1200
AAGTCATGTG TTGTCAATGT AAGTGTGATG TTTACACTAG TCTATGAAAG GCAGGGCAGA

      1210      1220      1230      1240      1250      1260
CGAGGGTAGT GTGCCAAGTA ACAGTGTGTC ATTATAGGTG TAAGTGTTGA GAATAAGACC

      1270      1280      1290      1300      1310      1320
ATTTTTGTTC ACAAATAGTA TGATGTAATC GGTGTCATAT TCGTATTGAG TACATTTGTC

      1330      1340      1350      1360
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<210> 13

<211> 329

<212> PRT

<213> Hordeum vulgare L.

<400> 13

Met	Asp	Ala	Gln	Ser	Lys	Glu	Val	Asp	Ala	Leu	Val	Gln	Lys	Ile	15
Thr	Gly	Leu	His	Ala	Ala	Ile	Ala	Lys	Leu	Pro	Ser	Leu	Ser	Pro	30
Ser	Pro	Asp	Val	Asp	Ala	Leu	Phe	Thr	Asp	Leu	Val	Thr	Ala	Cys	45
Val	Pro	Pro	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Ala	Pro	Glu	Ala	60
Gln	Ala	Met	Arg	Glu	Gly	Leu	Ile	Arg	Leu	Cys	Ser	Glu	Ala	Glu	75
Gly	Lys	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Ala	Ala	Phe	Asp	90
Asn	Pro	Leu	Asp	His	Leu	Gly	Val	Phe	Pro	Tyr	Tyr	Ser	Asn	Tyr	105

Ile	Asn	Leu	Ser	Lys	Leu	Glu	Tyr	Glu	Leu	Leu	Ala	Arg	Tyr	Val	120
Pro	Gly	Gly	Ile	Ala	Pro	Ala	Arg	Val	Ala	Phe	Ile	Gly	Ser	Gly	135
Pro	Leu	Pro	Phe	Ser	Ser	Tyr	Val	Leu	Ala	Ala	Arg	His	Leu	Pro	150
Asp	Thr	Val	Phe	Asp	Asn	Tyr	Val	Pro	Val	Arg	Ala	Ala	Asn	Asp	165
Arg	Ala	Thr	Arg	Leu	Phe	Arg	Ala	Asp	Lys	Asp	Val	Gly	Ala	Arg	180
Met	Ser	Phe	His	Thr	Ala	Asp	Val	Ala	Asp	Leu	Thr	Asp	Glu	Leu	195
Ala	Thr	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Ala	210
Ala	Glu	Asp	Lys	Gly	Gln	Gly	Asp	Pro	His	Leu	Gly	Ala	His	Met	225
Ala	Asp	Gly	Ala	Ala	Leu	Val	Arg	Ser	Ala	His	Gly	Ala	Arg	Gly	240
Phe	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Gln	Asp	Ile	Gly	Arg	Gly	Gly	255
Phe	Glu	Val	Leu	Ala	Val	Cys	His	Pro	Asp	Asp	Asp	Val	Val	Asn	270
Ser	Val	Ile	Ile	Ala	Gln	Lys	Ser	Lys	Asp	Met	Phe	Ala	Asn	Gly	285
Pro	Arg	Asn	Gly	Cys	Gly	Gly	Arg	Tyr	Ala	Arg	Gly	Thr	Val	Pro	300
Val	Val	Ser	Pro	Pro	Cys	Arg	Phe	Gly	Glu	Met	Val	Ala	Asp	Val	315
Thr	Gln	Lys	Arg	Glu	Glu	Phe	Ala	Lys	Ala	Glu	Val	Ala	Phe		329

<210> 14
 <211> 1371
 <212> DNA
 <213> Hordeum vulgare L.
 <400> 14

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110	120	130	140	150
CAAGGAGGTC	GACGCCCTTG	TCCAGAAGAT	CACCGGCCTC	CACGCCGCCA
160	170	180	190	200
TCGCCAAGCT	GCCCTCGCTC	AGCCCGTCCC	CGGACGTCGA	CGCGCTCTTC
210	220	230	240	250
ACCGACCTGG	TCACCGCGTG	CGTGCCCCCG	AGCCCGTGG	ACGTGACCAA
260	270	280	290	300
GCTCGCCCCG	GAGGCGCAGG	CGATGCGGGA	GGGCCTCATC	CGCCTCTGCT
310	320	330	340	350
CCGAGGCCGA	GGGCAAGCTG	GAGGCGCACT	ACTCCGACAT	GCTCGCCGCC
360	370	380	390	400
TTCGACAACC	CGCTCGACCA	CCTCGGCGTC	TTCCCCTACT	ACAGCAACTA
410	420	430	440	450
CATCAACCTC	AGCAAGCTCG	AGTACGAGCT	CCTCGCGCGC	TACGTGCCCG
460	470	480	490	500
GCGGCATCGC	CCCGGCCCGC	GTCGCCCTTCA	TCGGCTCCGG	CCCGCTCCCG
510	520	530	540	550
TTCAGCTCCT	ACGTCCTCGC	CGCGCGCCAC	CTGCCCGACA	CCGTGTTCGA
560	570	580	590	600
CAACTACGTA	CCTGTGCGCG	CGGCCAACGA	CCGCGCGACC	AGGCTGTTCC
610	620	630	640	650
GCGCGGACAA	GGACGTCGGC	GCCCGCATGT	CGTTCCACAC	CGCCGACGTC
660	670	680	690	700
GCGGACCTCA	CCGACGAGCT	CGCTACGTAC	GACGTCGTCT	TCCTGGCCGC
710	720	730	740	750
GCTCGTGGGC	ATGGCCGCCG	AGGACAAGGG	CCAAGGTGAT	CCGCACCTTG
760	770	780	790	800
GCGCGCACAT	GGCGGACGGG	GCGGCCCTCG	TCCGCAGCGC	GCACGGGGCG
810	820	830	840	850

CGTGGGTTCC	TCTACCCGAT	CGTCGATCCC	CAAGACATTG	GTCGAGGCGG
860	870	880	890	900
GTTTCGAGGTG	CTCGCCGTGT	GTCACCCCGA	CGACGACGTG	GTGAACTCCG
910	920	930	940	950
TCATCATCGC	GCAGAAGTCT	AAGGACATGT	TTGCCAATGG	ACCTCGCAAC
960	970	980	990	1000
GGGTGTGGTG	GACGGTACGC	GCGAGGCACG	GTGCCGGTGG	TCAGCCCGCC
1010	1020	1030	1040	1050
CTGCAGGTC	GGCGAGATGG	TGGCAGACGT	GACCCAGAAG	AGAGAGGAGT
1060	1070	1080	1090	1100
TTGCCAAGGC	GGAAGTGGCC	TTCTGATTGC	TGCGAGGTCA	CCATCCGTAT
1110	1120	1130	1140	1150
GCCGCTGCTA	CCTTTCAATA	TCTTGCAATC	GTAGGTGGCG	ATTTTCCTAC
1160	1170	1180	1190	1200
TCTTGTTACG	ACCTTTCAAA	TCATATGTTG	TTTGTACCCA	ATAATGTAAG
1210	1220	1230	1240	1250
TGTGTTGCTT	ACACGCGCAT	GTCTTGTACA	CTCGGTCTCT	AGAAGGCAGG
1260	1270	1280	1290	1300
GCAGATCAAG	AGACTGTGCA	AAGGAAAAGA	AATGTGTGTT	GTTGTAGGTG
1310	1320	1330	1340	1350
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1360	1370	1380		
AAAAAAAAAA	AAAAAAAAAA	A		

<210> 15
 <211> 332
 <212> PRT
 <213> *Oryza sativa* L.
 <400> 15

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Ala	Gly	Leu	His	Ala	Ala	Ile	Ser	Lys	Leu	Pro	Ser	Leu	Ser	Pro	30
Ser	Ala	Glu	Val	Asp	Ala	Leu	Phe	Thr	Asp	Leu	Val	Thr	Ala	Cys	45
Val	Pro	Ala	Ser	Pro	Val	Asp	Val	Ala	Lys	Leu	Gly	Pro	Glu	Ala	60
Gln	Ala	Met	Arg	Glu	Glu	Leu	Ile	Arg	Leu	Cys	Ser	Ala	Ala	Glu	75
Gly	His	Leu	Glu	Ala	His	Tyr	Ala	Asp	Met	Leu	Ala	Ala	Phe	Asp	90
Asn	Pro	Leu	Asp	His	Leu	Ala	Arg	Phe	Pro	Tyr	Tyr	Gly	Asn	Tyr	105
Val	Asn	Leu	Ser	Lys	Leu	Glu	Tyr	Asp	Leu	Leu	Val	Arg	Tyr	Val	120
Pro	Gly	Ile	Ala	Pro	Thr	Arg	Val	Ala	Phe	Val	Gly	Ser	Gly	Pro	135
Leu	Pro	Phe	Ser	Ser	Leu	Val	Leu	Ala	Ala	His	His	Leu	Pro	Asp	150
Ala	Val	Phe	Asp	Asn	Tyr	Asp	Arg	Cys	Gly	Ala	Ala	Asn	Glu	Arg	165
Ala	Arg	Arg	Leu	Phe	Arg	Gly	Ala	Asp	Glu	Gly	Leu	Gly	Ala	Arg	180
Met	Ala	Phe	His	Thr	Ala	Asp	Val	Ala	Thr	Leu	Thr	Gly	Glu	Leu	195
Gly	Ala	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Ala	210
Ala	Glu	Glu	Lys	Ala	Gly	Val	Ile	Ala	His	Leu	Gly	Ala	His	Met	225
Ala	Asp	Gly	Ala	Ala	Leu	Val	Val	Arg	Thr	Ala	His	Gly	Ala	Arg	240
Gly	Phe	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Glu	Asp	Val	Arg	Arg	Gly	255
Gly	Phe	Asp	Val	Leu	Ala	Val	Cys	His	Pro	Glu	Asp	Glu	Val	Ile	270
Asn	Ser	Val	Ile	Val	Ala	Arg	Lys	Val	Gly	Ala	Ala	Ala	Ala	Ala	285
Ala	Ala	Ala	Arg	Arg	Asp	Glu	Leu	Ala	Asp	Ser	Arg	Gly	Val	Val	300
Leu	Pro	Val	Val	Gly	Pro	Pro	Ser	Thr	Cys	Cys	Lys	Val	Glu	Ala	315
Ser	Ala	Val	Glu	Lys	Ala	Glu	Glu	Phe	Ala	Ala	Asn	Lys	Glu	Leu	330
Ser	Val*														345

<210> 16

<211> 1372

<212> DNA

<213> *Oryza sativa* L.

<400> 16

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110	120	130	140	150
AGAACCAAGA	GGTCGCTGCC	CTGGTCGAGA	AGATCGCCGG	CCTCCACGCC
160	170	180	190	200
GCCATCTCCA	AGCTGCCGTC	GCTGAGCCCA	TCCGCCGAGG	TGGACGCGCT
210	220	230	240	250
CTTCACCGAC	CTCGTCACGG	CGTGCGTCCC	GGCGAGCCCC	GTCGACGTGG
260	270	280	290	300
CCAAGCTCGG	CCCGGAGGCG	CAGGCGATGC	GGGAGGAGCT	CATCCGCCTC
310	320	330	340	350
TGCTCCGCCG	CCGAGGGCCA	CCTCGAGGCG	CACTACGCCG	ACATGCTCGC
360	370	380	390	400
CGCCTTCGAC	AACCCGCTCG	ACCACCTCGC	CCGCTTCCCG	TACTACGGCA
410	420	430	440	450
ACTACGTCAA	CCTGAGCAAG	CTGGAGTACG	ACCTCCTCGT	CCGCTACGTC
460	470	480	490	500
CCCGGCATTG	CCCCCACCCG	CGTCGCCTTC	GTCGGGTCGG	GCCCGCTGCC
510	520	530	540	550
GTTTCAGCTCC	CTCGTGCTCG	CTGCGCACCA	CCTGCCGGAC	GCGGTGTTCG
560	570	580	590	600
ACAACCTACGA	CCGGTGCGGC	GCGGCCAACG	AGCGGGCGAG	GAGGCTGTTC
610	620	630	640	650
CGCGGCGCCG	ACGAGGGCCT	CGGCGCGCGC	ATGGCGTTCC	ACACCGCCGA
660	670	680	690	700
CGTGGCGACC	CTGACGGGGG	AGCTCGGCGC	GTACGACGTC	GTGTTCTTGG
710	720	730	740	750
CGGCGCTCGT	GGGCATGGCG	GCCGAGGAGA	AGGCCGGGGT	GATCGCGCAC
760	770	780	790	800
CTGGGCGCGC	ACATGGCGGA	CGGCGCGGCG	CTCGTCTGTC	GGACGGCGCA
810	820	830	840	850
CGGGGCGCGC	GGGTTCCTGT	ACCCGATCGT	CGATCCCGAG	GACGTCAGGC
860	870	880	890	900
GTGGCGGGTT	CGACGTTCTG	GCGGTGTGCC	ACCCGGAGGA	CGAGGTGATC
910	920	930	940	950
AACTCCGTCA	TCGTGCCCCG	CAAGGTCGGT	GCCGCCGCCG	CCGCCGCCGC
960	970	980	990	1000
GGCGCGCAGA	GACGAGCTCG	CGGACTCGCG	CGGCGTGGTT	CTGCCGGTGG
1010	1020	1030	1040	1050
TCGGGCCGCC	GTCCACGTGC	TGCAAGGTGG	AGGCGAGCGC	GGTTGAGAAG
1060	1070	1080	1090	1100
GCAGAAGAGT	TTGCCGCCAA	CAAGGAGCTG	TCCGTCTAAC	AGCCGGACGA
1110	1120	1130	1140	1150
TCGAAAGGCG	CACTATATTA	TGGCAATAAA	TCATTTGATT	ATACTTATGC
1160	1170	1180	1190	1200
TGCATTTGCG	AAGCTAAGGT	ATACTATGCA	AGCCATATGT	TTGTGTTCGT
1210	1220	1230	1240	1250

ACGTGTTGTT	TGGGACGTAC	AGTTGTGTTG	TTGTACGTCG	TGAAGTACTG
1260	1270	1280	1290	1300
AAGTGTTTAC	AGTAGATCAC	AAGTTCACAG	CAATCAATGA	GGACCCTGTA
1310	1320	1330	1340	1350
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<210> 17
 <211> 320
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 17

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Val	Asp	Thr	Leu	Phe	Gly	Gln	Leu	Val	Ser	Thr	Cys	Leu	Pro	Thr	45
Asp	Thr	Asn	Ile	Asp	Val	Thr	Asn	Met	Cys	Glu	Glu	Val	Lys	Asp	60
Met	Arg	Ala	Asn	Leu	Ile	Lys	Leu	Cys	Gly	Glu	Ala	Glu	Gly	Tyr	75
Leu	Glu	Gln	His	Phe	Ser	Thr	Ile	Leu	Gly	Ser	Leu	Gln	Glu	Asp	90
Gln	Asn	Pro	Leu	Asp	His	Leu	His	Ile	Phe	Pro	Tyr	Tyr	Ser	Asn	105
Tyr	Leu	Lys	Leu	Gly	Lys	Leu	Glu	Phe	Asp	Leu	Leu	Ser	Gln	His	120
Ser	Ser	His	Val	Pro	Thr	Lys	Ile	Ala	Phe	Val	Gly	Ser	Gly	Pro	135
Met	Pro	Leu	Thr	Ser	Ile	Val	Leu	Ala	Lys	Phe	His	Leu	Pro	Asn	150
Thr	Thr	Phe	His	Asn	Phe	Asp	Ile	Asp	Ser	His	Ala	Asn	Thr	Leu	165
Ala	Ser	Asn	Leu	Val	Ser	Arg	Asp	Pro	Asp	Leu	Ser	Lys	Arg	Met	180
Ile	Phe	His	Thr	Thr	Asp	Val	Leu	Asn	Ala	Thr	Glu	Ala	Leu	Asp	195
Gln	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Asp	Lys	210
Glu	Ser	Lys	Val	Lys	Ala	Ile	Glu	His	Leu	Glu	Lys	His	Met	Ala	225
Pro	Gly	Ala	Val	Leu	Met	Leu	Arg	Arg	Ala	His	Ala	Leu	Arg	Ala	240
Phe	Leu	Tyr	Pro	Ile	Val	Asp	Ser	Ser	Asp	Leu	Lys	Gly	Phe	Gln	255
Leu	Leu	Thr	Ile	Tyr	His	Pro	Thr	Asp	Asp	Val	Val	Asn	Ser	Val	270
Val	Ile	Ala	Arg	Lys	Leu	Gly	Gly	Pro	Thr	Thr	Pro	Gly	Val	Asn	285
Gly	Thr	Arg	Gly	Cys	Met	Phe	Met	Pro	Cys	Asn	Cys	Ser	Lys	Ile	300
His	Ala	Ile	Met	Asn	Asn	Arg	Gly	Lys	Lys	Asn	Met	Ile	Glu	Glu	315
Phe	Ser	Thr	Ile	Glu											320

<210> 18
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 <213> Arabidopsis thaliana
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ACGTGCTTAC	CCACGGATAC	AAACATCGAT	GTCACAAATA	TGTGTGAAGA	AGTCAAAGAC	180
ATGAGAGCTA	ATCTCATCAA	GCTTTGTGGT	GAAGCCGAAG	GTTATTTGGA	GCAACACTTC	240
TCCACAATTT	TGGGATCTTT	ACAAGAAGAC	CAAAACCCAC	TTGACCATTT	ACACATCTTT	300
CCTTACTACT	TCCAACACTT	CAAGCTAGGC	AAGCTCGAGT	TCGATCTCCT	GAGCCAACAC	360
TCAAGCCATG	TCCCCACCAA	GATTGCCTTC	GTGGGTTTCG	GTCCGATGCC	TCTCACATCC	420
ATCGTATTGG	CCAAGTTTCA	CCTCCCCAAC	ACGACGTTCC	ACAACTTTGA	CATCGACTCA	480
CACGCAAACA	CACTCGCTTC	AAACCTCGTC	TCTCGCGACC	CGGACCTCTC	AAAACGCATG	540
ATCTTCCACA	CAACGGACGT	ACTAAACGCA	ACCGAAGCCC	TTGACCAATA	TGACGTCGTT	600
TTCTTAGCGG	CGCTTGTAAG	GATGGACAAA	GAGTCAAAGG	TCAAAGCCAT	CGAGCACTTG	660
GAGAAACACA	TGGCTCCTGG	AGCTGTTCTT	ATGCTAAGGA	GGGCTCATGC	TCTCAGAGCT	720
TTCTTATATC	CAATCGTTGA	CTCGTCTGAT	CTCAAAGGCT	TTCAACTCTT	GACCATCTAT	780

CATCCAACCG	ATGACGTGGT	TAACTCGGTT	GTGATCGCAC	GTAAGCTCGG	TGGTCCGACC	840
ACGCCCCGGG	TTAATGGTAC	TCGTGGATGC	ATGTTTATGC	CTTGTAAGT	CTCCAAGATT	900
CACGCGATCA	TGAACAACCG	TGTAAGAAG	AATATGATCG	AGGAGTTTAG	TACCATCGAG	960
TAA						963

<210> 19
 <211> 320
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 19

Met	Ala	Cys	Gln	Asn	Asn	Leu	Val	Val	Lys	Gln	Ile	Met	Asp	Leu	15
Tyr	Asn	Gln	Ile	Ser	Asn	Leu	Glu	Ser	Leu	Lys	Pro	Ser	Lys	Asn	30
Val	Asp	Thr	Leu	Phe	Arg	Gln	Leu	Val	Ser	Thr	Cys	Leu	Pro	Thr	45
Asp	Thr	Asn	Ile	Asp	Val	Thr	Glu	Ile	His	Asp	Glu	Lys	Val	Lys	60
Asp	Met	Arg	Ser	His	Leu	Ile	Lys	Leu	Cys	Gly	Glu	Ala	Glu	Gly	75
Tyr	Leu	Glu	Gln	His	Phe	Ser	Ala	Ile	Leu	Gly	Ser	Phe	Glu	Asp	90
Asn	Pro	Leu	Asn	His	Leu	His	Ile	Phe	Pro	Tyr	Tyr	Asn	Asn	Tyr	105
Leu	Lys	Leu	Gly	Lys	Leu	Glu	Phe	Asp	Leu	Leu	Ser	Gln	His	Thr	120
Thr	His	Val	Pro	Thr	Lys	Val	Ala	Phe	Ile	Gly	Ser	Gly	Pro	Met	135
Pro	Leu	Thr	Ser	Ile	Val	Leu	Ala	Lys	Phe	His	Leu	Pro	Asn	Thr	150
Thr	Phe	His	Asn	Phe	Asp	Ile	Asp	Ser	His	Ala	Asn	Thr	Leu	Ala	165
Ser	Asn	Leu	Val	Ser	Arg	Asp	Ser	Asp	Leu	Ser	Lys	Arg	Met	Ile	180
Phe	His	Thr	Thr	Asp	Val	Leu	Asn	Ala	Lys	Glu	Gly	Leu	Asp	Gln	195
Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Asp	Lys	Glu	210
Ser	Lys	Val	Lys	Ala	Ile	Glu	His	Leu	Glu	Lys	His	Met	Ala	Pro	225
Gly	Ala	Val	Val	Met	Leu	Arg	Ser	Ala	His	Gly	Leu	Arg	Ala	Phe	240
Leu	Tyr	Pro	Ile	Val	Asp	Ser	Cys	Asp	Leu	Lys	Gly	Phe	Glu	Val	255
Leu	Thr	Ile	Tyr	His	Pro	Ser	Asp	Asp	Val	Val	Asn	Ser	Val	Val	270
Ile	Ala	Arg	Lys	Leu	Gly	Gly	Ser	Asn	Gly	Ala	Arg	Gly	Ser	Gln	285
Ile	Gly	Arg	Cys	Val	Val	Met	Pro	Cys	Asn	Cys	Ser	Lys	Val	His	300
Ala	Ile	Leu	Asn	Asn	Arg	Gly	Met	Glu	Lys	Asn	Leu	Ile	Glu	Glu	315
Phe	Ser	Ala	Ile	Glu											320

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 <213> Arabidopsis thaliana
 <400> 20

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ACGTGCTTAC	CAACGGACAC	GAACATCGAT	GTCACAGAGA	TACACGATGA	AAAAGTCAAA	180
GACATGAGAT	CTCATCTCAT	CAAGCTTTGT	GGTGAAGCCG	AAGGTTATTT	AGAGCAACAC	240
TTTTCAGCAA	TCTTAGGCTC	TTTTGAAGAC	AACCCTCTAA	ACCATTTACA	CATCTTCCCC	300
TATTACAACA	ACTATCTCAA	ACTAGGCAAA	CTCGAATTCTG	ATCTCCTTTC	TCAGCACACA	360
ACCCATGTCC	CGACCAAGT	CGCCTTTATT	GGTTCCGGTC	CGATGCCACT	TACTTCCATC	420
GTCTTGCCCA	AGTTCCACCT	CCCCAACACA	ACGTTCCACA	ACTTCGACAT	CGACTCACAC	480
GCCAACACAC	TCGCTTCAAA	CCTCGTTTCT	CGTGATTCTG	ACCTTTCCAA	ACGCATGATT	540
TTCCACACAA	CTGATGTATT	AAACGCTAAG	GAGGGGTTAG	ACCAATACGA	TGTTGTTTTTC	600
TTGGCAGCTC	TTGTTGGGAT	GGATAAGAG	TCAAAGGTCA	AAGCTATTGA	GCATTTAGAG	660
AAGCATATGG	CCCCTGGAGC	TGTGGTGATG	CTAAGAAGTG	CTCATGGTCT	TAGAGCTTTC	720
TTGTATCCAA	TCGTTGACTC	TTGTGATCTT	AAAGGGTTTG	AGGTGTTAAC	CATTTATCAT	780
CCGTCTGACG	ACGTGGTTAA	TTCGGTGGTC	ATCGCACGTA	AGCTTGGTGG	TTCAAATGGA	840
GCTCGAGGCA	GCCAGATCGG	ACGGTGTGTG	GTTATGCCTT	GTAATTGCTC	TAAGGTCCAC	900
GCGATCTTGA	ACAATCGTGG	TATGGAGAAG	AATTTGATCG	AGGAGTTTAG	TGCCATCGAG	960

<210> 21
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 <212> PRT
 <213> Arabidopsis thaliana
 <400> 21

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Tyr	Glu	Lys	Ile	Ser	Lys	Leu	Glu	Ser	Leu	Lys	Pro	Ser	Glu	Asp	30
Val	Asn	Ile	Leu	Phe	Lys	Gln	Leu	Val	Ser	Thr	Cys	Ile	Pro	Pro	45
Asn	Pro	Asn	Ile	Asp	Val	Thr	Lys	Met	Cys	Asp	Arg	Val	Gln	Glu	60
Ile	Arg	Leu	Asn	Leu	Ile	Lys	Ile	Cys	Gly	Leu	Ala	Glu	Gly	His	75
Leu	Glu	Asn	His	Phe	Ser	Ser	Ile	Leu	Thr	Ser	Tyr	Gln	Asp	Asn	90
Pro	Leu	His	His	Leu	Asn	Ile	Phe	Pro	Tyr	Tyr	Asn	Asn	Tyr	Leu	105
Lys	Leu	Gly	Lys	Leu	Glu	Phe	Asp	Leu	Leu	Glu	Gln	Asn	Leu	Asn	120
Gly	Phe	Val	Pro	Lys	Ser	Val	Ala	Phe	Ile	Gly	Ser	Gly	Pro	Leu	135
Pro	Leu	Thr	Ser	Ile	Val	Leu	Ala	Ser	Phe	His	Leu	Lys	Asp	Thr	150
Ile	Phe	His	Asn	Phe	Asp	Ile	Asp	Pro	Ser	Ala	Asn	Ser	Leu	Ala	165
Ser	Leu	Leu	Val	Ser	Ser	Asp	Pro	Asp	Ile	Ser	Gln	Arg	Met	Phe	180
Phe	His	Thr	Val	Asp	Ile	Met	Asp	Val	Thr	Glu	Ser	Leu	Lys	Ser	195
Phe	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Asn	Lys	Glu	210
Glu	Lys	Val	Lys	Val	Ile	Glu	His	Leu	Gln	Lys	His	Met	Ala	Pro	225
Gly	Ala	Val	Leu	Met	Leu	Arg	Ser	Ala	His	Gly	Pro	Arg	Ala	Phe	240
Leu	Tyr	Pro	Ile	Val	Glu	Pro	Cys	Asp	Leu	Gln	Gly	Phe	Glu	Val	255
Leu	Ser	Ile	Tyr	His	Pro	Thr	Asp	Asp	Val	Ile	Asn	Ser	Val	Val	270
Ile	Ser	Lys	Lys	His	Pro	Val	Val	Ser	Ile	Gly	Asn	Val	Gly	Gly	285
Pro	Asn	Ser	Cys	Leu	Leu	Lys	Pro	Cys	Asn	Cys	Ser	Lys	Thr	His	300
Ala	Lys	Met	Asn	Lys	Asn	Met	Met	Ile	Glu	Glu	Phe	Gly	Ala	Arg	315
Glu	Glu	Gln	Leu	Ser											320

<210> 22
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 <212> DNA
 <213> Arabidopsis thaliana
 <400> 22

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ACATGCATAC	CACCAAACCC	TAACATCGAT	GTCACCAAGA	TGTGTGACAG	AGTCCAAGAG	180
ATTCGACTTA	ATCTCATCAA	GATTTGTGGT	CTAGCCGAAG	GTCACCTAGA	AAACCATTTC	240
TCTTCGATCT	TGACCTCTTA	CCAAGACAAC	CCACTTCATC	ATTTAAACAT	TTTCCCTTAT	300
TACAACAAC	ATTTGAAACT	CGGAAAGCTC	GAGTTCGACC	TCCTCGAACA	AAACCTAAAT	360
GGCTTTGTCC	CAAAGAGTGT	GGCTTTTCATT	GGATCTGGTC	CTCTTCCTCT	CACTTCCATC	420
GTTCTTGCTT	CATTCCATCT	CAAAGACACA	ATCTTTTACA	ACTTTGACAT	CGACCCATCA	480
GCGAACTCAC	TCGCTTCTCT	TCTGGTTTCC	TCTGATCCAG	ACATCTCTCA	ACGCATGTTC	540
TTCCACACCG	TTGATATAAT	GGACGTGACA	GAGAGCTTAA	AGAGCTTTGA	TGTCGTGTTT	600
CTAGCTGCTC	TTGTTGGAAT	GAACAAAGAG	GAGAAAGTTA	AAGTGATCGA	GCATCTGCAG	660
AAACACATGG	CTCCTGGTGC	TGTGCTCATG	CTTAGGAGTG	CTCATGGTCC	GAGAGCGTTT	720
CTTTATCCGA	TCGTTGAGCC	GTGTGATCTT	CAGGGGTTCG	AGGTTTTGTC	TATTTATCAC	780
CCAACAGATG	ATGTTATCAA	CTCCGTGGTG	ATCTCTAAAA	AGCATCCAGT	TGTTTCAATT	840
GGGAATGTTG	GTGGTCCTAA	TTCATGCTTG	CTCAAGCCTT	GCAACTGTTC	CAAGACCCAC	900
GCGAAAATGA	ACAAGAACAT	GATGATCGAG	GAGTTCGGAG	CTAGGGAGGA	ACAGTTGTCT	960
TAA						963